RAW SEQUENCE LISTING   DATE: 07/08/2002
PATENT APPLICATION: US/10/087,188   TIME: 10:09:37

Input Set : A:\PM4978.txt
Output Set: N:\CRF3\07082002\J087188.raw

```
   4 <110> APPLICANT: Rose, Steven L.
   5        Oh, Esther H.
   6        Walsh, Michael
   8 <120> TITLE OF INVENTION: Methods of Diagnosing Liver Fibrosis
  11 <130> FILE REFERENCE: P-PM 4978
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/087,188
C--> 13 <141> CURRENT FILING DATE: 2002-02-28
  13 <150> PRIOR APPLICATION NUMBER: US 10/087,188
  14 <151> PRIOR FILING DATE: 2002-02-28
  16 <160> NUMBER OF SEQ ID NOS: 4
  18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  20 <210> SEQ ID NO: 1
  21 <211> LENGTH: 2041
  22 <212> TYPE: DNA
  23 <213> ORGANISM: Homo sapiens
  25 <220> FEATURE:
  26 <221> NAME/KEY: CDS
  27 <222> LOCATION: (1)...(1932)
  29 <400> SEQUENCE: 1
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  31 Pro Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro His Cys
  32  1               5                  10                  15
  34 atc tgt gca aac ggg cgg caa act gtg tcc tgg gca gta acc cca aag    96
  35 Ile Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys
  36              20                  25                  30
  38 tca tta gga aat gtg aat ttc act gtg agc gca gag gca cta gag tct   144
  39 Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser
  40              35                  40                  45
  42 caa gag ctg tgt ggg act gag gtg cct tca gtt cct gaa cac gga agg   192
  43 Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg
  44          50                  55                  60
  46 aaa gac aca gtc atc aag cct ctg ttg gtt gaa cct gaa gga cta gag   240
  47 Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu
  48  65                  70                  75                  80
  50 aag gaa aca aca ttc aac tcc cta ctt tgt cca tca ggt ggt gag gtt   288
  51 Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val
  52              85                  90                  95
  54 tct gaa gaa tta tcc ctg aaa ctg cca cca aat gtg gta gaa gaa tct   336
  55 Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser
  56             100                 105                 110
  58 gcc cga gct tct gtc tca gtt ttg gga gac ata tta ggc tct gcc atg   384
  59 Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met
  60         115                 120                 125
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62  caa aac aca caa aat ctt ctc cag atg ccc tat ggc tgt gga gag cag    432
63  Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln
64      130             .           135             140
66  aat atg gtc ctc ttt gct cct aac atc tat gta ctg gat tat cta aat    480
67  Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn
68  145             150             155             160
70  gaa aca cag cag ctt act cca gag atc aag tcc aag gcc att ggc tat    528
71  Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser Lys Ala Ile Gly Tyr
72              165             170             175
74  ctc aac act ggt tac cag aga cag ttg aac tac aaa cac tat gat ggc    576
75  Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly
76              180             185             190
78  tcc tac agc acc ttt ggg gag cga tat ggc agg aac cag ggc aac acc    624
79  Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr
80              195             200             205
82  tgg ctc aca gcc ttt gtt ctg aag act ttt gcc caa gct cga gcc tac    672
83  Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr
84      210             215             220
86  atc ttc atc gat gaa gca cac att acc caa gcc ctc ata tgg ctc tcc    720
87  Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser
88  225             230             235             240
90  cag agg cag aag gac aat ggc tgt ttc agg agc tct ggg tca ctg ctc    768
91  Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu
92              245             250      .          255
94  aac aat gcc ata aag gga gga gta gaa gat gaa gtg acc ctc tcc gcc    816
95  Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala
96              260             265             270
98  tat atc acc atc gcc ctt ctg gag att cct ctc aca gtc act cac cct    864
99  Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro
100         275             280             285
102 gtt gtc cgc aat gcc ctg ttt tgc ctg gag tca gcc tgg aag aca gca    912
103 Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala
104     290             295             300
106 caa gaa ggg gac cat ggc agc cat gta tat acc aaa gac ctg ctg gcc    960
107 Gln Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Asp Leu Leu Ala
108 305             310             315             320
110 tat gct ttt gcc ctg gca ggt aac cag gac aag agg aag gaa gta ctc   1008
111 Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu
112             325             330             335
114 aag tca ctt aat gag gaa gct gtg aag aaa gac aac tct gtc cat tgg   1056
115 Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp
116             340             345             350
118 gag cgc cct cag aaa ccc aag gca cca gtg ggg gat ttt tac gaa ccc   1104
119 Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly Asp Phe Tyr Glu Pro
120         355             360             365
122 cag gct ccc tct gct gag gtg gag atg aca tcc tat gtg ctc ctc gct   1152
123 Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala
124     370             375             380
126 tat ctc acg gcc cag cca gcc cca acc tcg gag gac ctg acc tct gca   1200
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127 Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala
128 385             390             395             400
130 acc aac atc gtg aag tgg atc acg aag cag cag aat gcc cag ggc ggt    1248
131 Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly
132             405             410             415
134 ttc tcc tcc acc cag gac aca gtg gtg gct ctc cat gct ctg tcc aaa    1296
135 Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys
136             420             425             430
138 tat gga gca gcc aca ttt acc agg act ggg aag gct gca cag gtg act    1344
139 Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr
140         435             440             445
142 atc cag tct tca ggg aca ttt tcc agc aaa ttc caa gtg gac aac aac    1392
143 Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn
144         450             455             460
146 aac cgc ctg tta ctg cag cag gtc tca ttg cca gag ctg cct ggg gaa    1440
147 Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu
148 465             470             475             480
150 tac agc atg aaa gtg aca gga gaa gga tgt gtc tac ctc cag aca tcc    1488
151 Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser
152             485             490             495
154 ttg aaa tac aat att ctc cca gaa aag gaa gag ttc ccc ttt gct tta    1536
155 Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu
156             500             505             510
158 gga gtg cag act ctg cct caa act tgt gat gaa ccc aaa gcc cac acc    1584
159 Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr
160         515             520             525
162 agc ttc caa atc tcc cta agt gtc agt tac aca ggg agc cgc tct gcc    1632
163 Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala
164         530             535             540
166 tcc aac atg gcg atc gtt gat gtg aag atg gtc tct ggc ttc att ccc    1680
167 Ser Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro
168 545             550             555             560
170 ctg aag cca aca gtg aaa atg ctt gaa aga tct aac cat gtg agc cgg    1728
171 Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg
172             565             570             575
174 aca gaa gtc agc agc aac cat gtc ttg att tac ctt gat aag gtg tca    1776
175 Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser
176             580             585             590
178 aat cag aca ctg agc ttg ttc ttc acg gtt ctg caa gat gtc cca gta    1824
179 Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val
180             595             600             605
182 aga gat ctg aaa cca gcc ata gtg aaa gtc tat gat tac tac gag acg    1872
183 Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr
184         610             615             620
186 gat gag ttt gca att gct gag tac aat gct cct tgc agc aaa gat ctt    1920
187 Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu
188 625             630             635             640
190 gga aat gct tga agaccacaag gctgaaaagt gctttgctgg agtcctgttc        1972
191 Gly Asn Ala  *
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194  tcagagctcc acagaagaca cgtgtttttg tatctttaaa gacttgatga ataaacactt 2032
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198  <211> LENGTH: 643
199  <212> TYPE: PRT
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206              20                  25                  30
207  Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser
208          35                  40                  45
209  Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg
210      50                  55                  60
211  Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu
212  65                  70                  75                  80
213  Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val
214                  85                  90                  95
215  Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser
216              100                 105                 110
217  Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met
218          115                 120                 125
219  Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln
220      130                 135                 140
221  Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn
222  145                 150                 155                 160
223  Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser Lys Ala Ile Gly Tyr
224                  165                 170                 175
225  Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly
226              180                 185                 190
227  Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr
228          195                 200                 205
229  Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr
230      210                 215                 220
231  Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser
232  225                 230                 235                 240
233  Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu
234                  245                 250                 255
235  Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala
236              260                 265                 270
237  Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro
238          275                 280                 285
239  Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala
240      290                 295                 300
241  Gln Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Asp Leu Leu Ala
242  305                 310                 315                 320
243  Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu
244                  325                 330                 335
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```
245 Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp
246             340             345             350
247 Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly Asp Phe Tyr Glu Pro
248         355             360             365
249 Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala
250     370             375             380
251 Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala
252 385             390             395             400
253 Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly
254             405             410             415
255 Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys
256         420             425             430
257 Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr
258     435             440             445
259 Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn
260     450             455             460
261 Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu
262 465             470             475             480
263 Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser
264             485             490             495
265 Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu
266         500             505             510
267 Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr
268     515             520             525
269 Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala
270     530             535             540
271 Ser Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro
272 545             550             555             560
273 Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg
274         565             570             575
275 Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser
276         580             585             590
277 Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val
278     595             600             605
279 Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr
280     610             615             620
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288 <211> LENGTH: 782
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
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293 <221> NAME/KEY: CDS
294 <222> LOCATION: (63)...(686)
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298 cc atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg    107
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VERIFICATION SUMMARY   DATE: 07/08/2002
PATENT APPLICATION: **US/10/087,188**   TIME: 10:09:38

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3